

## STIC Biotechnology Systems Branch

### CRF Problem Report

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 10/593,426  
Filing Date: 9/19/06  
Date Processed by STIC: 9/27/06

STIC Contact: Mark Spencer: Telephone: 571-272-2510; Fax: 571-273-0221

#### Nature of CRF Problem:

- ☐ (circle one) Damaged or Unreadable (for Unreadable, see attached)
- ☐ Blank (no files on CRF) (see attached)
- ☐ Empty file (filename present, but no bytes in file) (see attached)
- ☐ Wrong file saved to CRF (invention title, docket number, or applicant(s) do not match those in official application) (see attached)
- ☐ Not saved in ASCII text
- ☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
- ☐ Did not contain a Sequence Listing. (see attached sample)
- ☒ Other: Alpha numeric headings in sequence.

**PLEASE USE THE CHECKER VERSION 4.3.1 PROGRAM TO REDUCE ERRORS.  
SEE BELOW FOR ADDRESS:**

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,  
Alexandria, VA 22314

Revised 08/30/05

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER

10/593,426

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino Numbering The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences (OLD RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences (NEW RULES) Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220> Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

10/593,426  
(Sample of submitted file)

PAGE 1

SEQUENCE LISTING

<110> PAPES, Fabio  
GERHARDT, Isabel Rodrigues  
ARRUDA, Paulo

<120> CAMBIUM/XYLEM-PREFERRED PROMOTERS AND USES THEREOF

<130> ALEL 202.1 PCT

<140>  
<141>

<150> US 60/560,227  
<151> 2004-04-06

<160> 41

<170> PatentIn version 3.2

<200> SEQUENCE CHARACTERISTICS:

<210> SEQ ID NO 1

<211> LENGTH: 3035

<212> TYPE: DNA

<213> ORGANISM: Populus sp.

<220> FEATURE

<221> NAME/KEY: promoter

<222> LOCATION: (1)...(3035)

<223> OTHER INFORMATION: Sucrose synthase (SUSY) promoter

<400> SEQUENCE: 1

tcattgtccta tccaacggcg atgcaaactt cgctgtcccg cactttttca taggacgagg tgaagtttag 70

ctatatatct ttttttttta atttaaattg ttaattcttt atatttttat attcttttaa ttttatattt

140

ttatatatt ttgatatatt acatcaagaa taaattttta aaaaataatt tttaaattt acttaaccac

210

gcaatacata aaaaataata gaaccaccca acctaagaat acttgtcaat gcatagaagt acacctgcta

280

gttcttaaaa ccaacaaaag gaagcaaagt agatctctga gtcaaaaacc agaggaaacc atagaaacac

350

gdaataataa taataataat aataataata aaattaattt aacttggtgt aataataaaa ttaattta

420

tcacaagagt gtaactcaac tagtcatgtt cttaaatttat tctctagaga ttactagttt gagttttaca

490

aattttaagg ccaactgaaga tttatatagt cattaatttc agaatatata agattagttg agttacgtat

560

aaattgatta aaaaatcata ttaataaaaa taaaaaaatt aatttaaagg tttaagaaat caaattaaga

630

gaaagagtg gtgttttatt tttcatcgtg cctctctca acagacaagt agaagatga gagagagagg

700

gttaagaaat ggatttatga gaacattgac cacagggaaa gagagaagcg gttttgtgaa aggaacaatg

770

aagccacagg aaggtaaagc ggtaatgata tatttcacga atactaaaac tagaacaaca agttttttta

840

tcaattaaa ccacgagtg caggccgtct tctctgtgta taaaagggtc cttcttcttt ctcatttccc

910

attctcatct gcaaacttct cttttgcaat ctttctttct tgcgttctgt gtgttcgttg tgatttgtgt

980

pls see item #1 on error  
Summary sheet.

pls  
delete

pls delete,  
invalid  
numeric  
identifiers.

pls do not insert  
Alpha numeric headings  
in sequence.

These types  
of errors  
are seen  
globally  
throughout  
the sequence.

1050 tcttcttct tgtctattag cttgtccccc cgtccgactg ctttctgtat ttattctggc attaaactta  
 1120 aggtaaagat ccctcaacta tcccaagcaa tttattctgt ttttatgtga tcttgaggga tcttcctctt  
 1190 ggatgcgctt tttatTTTTT cttcctcctt cttcctgctc cttcttacct tgtatctgat cccccagacg  
 1260 aaaatgtttt ttgttttttt aattagctca acaaatacaa aacattcaca taataacaca gctcgaaaga  
 1330 aatctgatac agttttaatc tgttgtatTT taaaaatcat tacagttcat gcatgctgat actttacat  
 1400 gtcataaat taaatcccag catccttttc catagccaaa gaaggatcag cagcatgctg atagtttacc  
 1470 atgtcatgaa attaaatccc agcatccttt tccatagcca aagaaagatc agcagcatgc ttgcttatac  
 1540 aaggctcttg cttgcttatt aaggccactg aaacatcatc atcgtcataa ctatgataga acccgctac  
 1610 tgccggcatt gaaaacatca tcaactagtgt ctctacatta aaaaacaccc actgtctaatt ttcctatttt  
 1680 tttactctta aaatgtcttt cggcttgagc tctcgggct ccacggatgg caactgctgt attatatata  
 1750 tatatatata tatatatata tatatatata tatatatata tatatatata tatatttocc tgttggctac  
 1820 atagacctgt taataccgta taaatagata atattaatat atagaattca tgtatctttc cgagattaag  
 1890 cgatgccgta taaataatat taatatcttt gaatcagtat gtatattaat taaaattaat ttttttcaaa  
 1960 gtaattttta gagcgcattt tcaacatcca tttagttttt ttttaataat aaatctctct ttgcattaat  
 2030 cctaactgtt gaacttagta aattaaaaaa aggaaaatac ctttttcacc aatatagaat caatgaacag  
 2100 cactagtttg cttgaaataa aaataaaaaa aaaatctaatt aagacatttc gaaatcatcc ttatccgcaa  
 2170 atcactacat tagtatagta tcttgaaaga taagcaagga tcatgcaagt ttataataat taaacttaaa  
 2240 acgtactatg acgtgtgcat cattcattca ttctgcatga aactctccac aagtctagcc ttgcatcat  
 2310 tcattctact tcattttatt ttttcctcta atggtttoga ttgatttttc tttcttagag tctggtcttt  
 2380 tagttcaact ttacatgttt taggctcgta ttttgagaga aaaaaagaa aaaagtatgc agatcatgat  
 2450 tctgcaaaat actgaactag tgttctgatg aattaacatg tagcatgtat aatgctggaa gaactaaaga  
 2520 gcagttgggc tgccatgacc aaaagaaact tcgactgatt ataaatgtca aaacttgggc ccattctttg  
 2590 gtttctgtct gttgttttat gccatggcaa aactctgctt atttttcaac gtccaacgct aaatgggaga  
 2660 ggtttaaatt ctattgttat gtctaaacca cgtgggtggt atctatatct gaccgaacat tcaagctttt  
 2730 ggtattccac aagaagggtt ttctctcttc tttcttttca taattgtaat gtgtttaatt tgtttcttgc  
 2800 ccaataatct tctctgcttc aaactaactt taattgttcg atctcttgcg ttattttaga catgtgcaat  
 2870 cacctttcac tgttgaaaaa atgggtgggt aggtgaggtg gtaggttttg aagtcttcta gaataatgtg  
 2940 gtttctctgt tgctcttgac ttcttcttgt agatcatttc tggctggcta agctatccat accccccgcg  
 cctacaaat aatattgagt tgttgctggt cttaattcct attatctggt attactccca ctgattgctt

Same  
 errors

See  
 item

# 1

on error

Summary

Sheet

3010  
~~ttt~~gtttctc ttaaggagct atggc  
3035

← Same  
error

10/593,426

page 4

<200> SEQUENCE CHARACTERISTICS: *pls delete, invalid numeric identifier*  
<210> SEQ ID NO 13  
<211> LENGTH 31  
<212> TYPE: DNA  
<213> ORGANISM/SOURCE synthetic *Invalid response*  
<221> NAME/KEY: primer/oligonucleotide *insert online <223>*  
<400> SEQUENCE: 13  
(5) GCCATAGCTC CTTAAGAGAA ACAGAAAGCA A -3' *delete*

*delete*

*pls use lowercase*

F.Y.I:

*See item #10 on error summary sheet.*

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

<213> responses CAN ONLY be either Artificial/Unknown or Genus/Species,